

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:37:02 ; Search time 176 Seconds  
(without alignments)  
2228.708 Million cell updates/sec

Title: US-10-733-368-35

Perfect score: 4081

Sequence: 1 MIWRSRAGAEFLSMALMEW.....QAFNAKLPTMTDYDTTKLCS 766

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*\*

2: uniprot\_trembl:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4081	100.0	766	2 Q76B58	Q76B58 homo sapien
2	4009	98.2	766	2 Q8K0R9	Q8K0R9 mus musculus
3	3998	98.0	766	2 Q8K1M7	Q8K1M7 rattus norv
4	2368	72.7	783	2 Q6DFI8	Q6DFI8 mus musculus
5	2363	72.6	788	2 Q80T96	Q80T96 mus musculus
6	2362	72.6	781	2 Q95560	Q95560 homo sapien
7	2362	72.6	783	2 Q8N360	Q8N360 homo sapien
8	2362	72.6	783	2 Q8K1M8	Q8K1M8 rattus norv
9	2362	72.6	791	2 Q9C0B6	Q9C0B6 homo sapien
10	2474.5	60.6	678	2 Q6ZWC1	Q6ZWC1 homo sapien
11	2184	53.5	761	2 Q7Z2R3	Q7Z2R3 gallus gall
12	2161	53.0	761	2 Q60477	Q60477 homo sapien
13	2161	53.0	761	2 Q6P1A0	Q6P1A0 homo sapien
14	2155.5	52.8	760	2 Q920P3	Q920P3 m bmp/retin
15	2151.5	52.7	760	2 Q8C1C9	Q8C1C9 mus musculus
16	2136.5	52.4	760	2 Q925T8	Q925T8 rattus norv
17	2128	52.1	761	2 Q9QXL0	Q9QXL0 mus musculus
18	1434.5	35.2	532	2 Q9SLG0	Q9SLG0 homo sapien
19	1224.5	30.0	476	2 Q61P06	Q61P06 homo sapien
20	1142	28.0	218	2 Q95726	Q95726 homo sapien
21	1026	25.1	378	2 Q812P0	Q812P0 mus musculus
22	970.5	23.8	320	2 Q8WU22	Q8WU22 homo sapien
23	967.5	23.7	320	2 Q80ZL2	Q80ZL2 mus musculus
24	901	22.1	206	2 Q7LCZ9	Q7LCZ9 homo sapien
25	720.5	17.7	228	2 Q8WX56	Q8WX56 homo sapien
26	175	4.3	72	2 Q920P4	Q920P4 mus musculus
27	153	3.7	587	1 C08B_ONCMY	Q90X85 oncothynchu
28	141.5	3.5	1460	2 Q6KH19	Q6KH19 mycoplasma
29	135.5	3.3	684	1 YMW5_YEAST	O04779 saccharomyc
30	134.5	3.3	799	2 Q6B1N0	Q6B1N0 debaryomyc
31	133	3.3	1004	2 Q7Q4Q2	Q7Q4Q2 anopheles g

Q7VYV7 cryptospori  
Q661Q6 borellia ga  
Q9QJ37 human herpe  
Q91J75 arabidopsis  
Q9TUG3 sus scrofa  
Q6BNA0 debaryomyc  
Q6CVH9 kluyveromyc  
Q869Q5 dictyosteli  
P10843 homo sapien  
Q6P3T5 homo sapien  
Q6LFD0 plasmodium  
Q81B63 plasmodium  
Q6VU88 oryza sativ  
Q7CQ89 rattus norv

## ALIGNMENTS

### RESULT 1

Q76B58 PRELIMINARY; PRT; 766 AA.  
ID Q76B58  
AC Q76B58;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE DECCRL-like.  
GN Name=DECCRL;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Imoto I., Inazawa J.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB111893; BAD04066.1; -  
DR InterPro: IPR001862; MAC\_perforin.  
DR Pfam: PF01823; MACPF; 1.  
DR SMART: SM00457; MACPF; 1.  
SQ SEQUENCE 766 AA; 8844 MW; D325EB7E9F416FB3 CRC64;

Query Match 100.0%; Score 4081; DB 2: Length 766;  
Best Local Similarity 100.0%; Pred. No. 2.2e-285;  
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MIWRSRAGAEFLSMALMEWIALSLHCWLVAAVSDQHATSPFDWLLSDKGPFRHSQBY 60  
DB 1 MIWRSRAGAEFLSMALMEWIALSLHCWLVAAVSDQHATSPFDWLLSDKGPFRHSQBY 60  
QY 61 TDFVDRSQGSTRYKIYREFGRWKVNLAVERNFLGSPPLAPEFFRNIRLLGRRPTL 120  
DB 61 TDFVDRSQGSTRYKIYREFGRWKVNLAVERNFLGSPPLAPEFFRNIRLLGRRPTL 120  
QY 121 QOITENLIKKGTHFLSATLGGESLTIYVDRKLSKRAEGSDSTNSSVLTLELHQL 180  
DB 121 QOITENLIKKGTHFLSATLGGESLTIYVDRKLSKRAEGSDSTNSSVLTLELHQL 180  
QY 181 AASYFIDRSDTLRLHHIQAISTAIVTETRTGPGCSNYDNLDSSVSVLQSPENKQL 240  
DB 181 AASYFIDRSDTLRLHHIQAISTAIVTETRTGPGCSNYDNLDSSVSVLQSPENKQL 240  
QY 241 QGLQVLLPDYLOERFVQAALSYACNSEGEFICKENDCWCCHGPKFPCNCPSMDIQAME 300  
DB 241 QGLQVLLPDYLOERFVQAALSYACNSEGEFICKENDCWCCHGPKFPCNCPSMDIQAME 300  
QY 301 ENLLRIITETWKVNSDFEESDEFKLFMKRLPMNYFLNTSTIMHLWTMDSNFORRYEQLN 360  
DB 301 ENLLRIITETWKVNSDFEESDEFKLFMKRLPMNYFLNTSTIMHLWTMDSNFORRYEQLN 360  
QY 361 SMKOLFKAQKIVHKLFSLSKRCHKQPLISLPRTSTYWLTRIQSFLYCNENGLLSGFS 420  
DB 361 SMKOLFKAQKIVHKLFSLSKRCHKQPLISLPRTSTYWLTRIQSFLYCNENGLLSGFS 420

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QY 421 BETHSCTCPNDQVCTAFLEPCTVGDASACLTCPAPDNTRCGTCTGNTGMYLSSQGLCKEVAE 480
DB 421 EETHSCTCPNDQVCTAFLEPCTVGDASACLTCPAPDNTRCGTCTGNTGMYLSSQGLCKEVAE 480
QY 481 STDHYIGFETDLODLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRMLLTLSKN 540
DB 481 STDHYIGFETDLODLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRMLLTLSKN 540
QY 541 KYKSSLVHMLILGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWPVSNSFPDWERTK 600
DB 541 KYKSSLVHMLILGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWPVSNSFPDWERTK 600
QY 601 LDLPLOQYNWTLTLGNKWKTFETVHIYLSRSIKNSGPNESIIYVEPLEFIDPSRNLYG 660
DB 601 LDLPLOQYNWTLTLGNKWKTFETVHIYLSRSIKNSGPNESIIYVEPLEFIDPSRNLYG 660
QY 661 MKINNIQVFGYSMHFDEPAIRDILQDYPYTOGSODSALLQLLEIRDRVNLSPPGQRR 720
DB 661 MKINNIQVFGYSMHFDEPAIRDILQDYPYTOGSODSALLQLLEIRDRVNLSPPGQRR 720
QY 721 LDLPFCLLRHRLKLSSTSEVVRISQALQAFNAKLPTNDYDITTKLCS 766
DB 721 LDLPFCLLRHRLKLSSTSEVVRISQALQAFNAKLPTNDYDITTKLCS 766

RESULT 2
Q8K0R9 PRELIMINARY; PRT; 766 AA.
ID Q8K0R9 AC Q8K0R9;
AC Q8K0R9;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE RIKEN cDNA B830045N13.
GN Name=B830045N13Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX Strausberg R.;
RA Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030498; AAH30498.1; -
DR MGD; MGI:2443035; B830045N13Rik.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
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DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 766 AA; 88482 MW; 15BC4F2DAF813B71 CRC64;

Query Match 98.2%; Score 4009; DB 2; Length 766;
Best Local Similarity 97.8%; Pred. No. 3 4e-280;
Matches 749; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 MIWRSAGAEFLSMALWENIALSLHCWVLA VAAVSDQHATSPFDWLLSDKGFHRSQEY 60
DB 1 MIWRRAGAELSSMALWENI VLSLHCWVLA VAAVSDQHATSPFDWLLSDKGFHRSQEY 60
QY 61 TDFVRSRGFGSTRYKIYREFGRKWNVLAVERRFLGSPPLAPAEFFNRILRGRRPTL 120
DB 61 TDFVRSRGFGSTRYKIYREFGRKWNVLAVERRFLGSPPLAPAEFFNRILRGRRPTL 120
QY 121 QOITENLIKGYTHFLSATLGGESLTI FVDRKRLSKRAEGSDSTNSSSVLTLETHQL 180
DB 121 QOITENLIKGYTHFLSATLGGESLTI FVDRKRLSKRAEGSDSTNSSSVLTLETHQL 180
QY 181 AASYFIDRSTLRLHHIOIASTAIKVTRTGPGLGCSNYDNLDVSSVLVQSPENKIQL 240
DB 181 AASYFIDRSTLRLHHIOIASTAIKVTRTGPGLGCSNYDNLDVSSVLVQSPENKIQL 240
QY 241 QGLQVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCPCGKPEPCNCPMDIOAME 300
DB 241 QGLQVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCPCGKPEPCNCPMDIOAME 300
QY 301 ENLLRITETWKAYNSDFEESDEFKLFMKELPNYI FLNTSTIMHLWTMDSNFQRRYEQLEN 360
DB 301 ENLLRITETWKAYNSDFEESDEFKLFMKELPNYI FLNTSTIMHLWTMDSNFQRRYEQLEN 360
QY 361 SMKQFLKAQKIVHKLFSLSKCKHQPLISLPRQRTSTTWLTRIQSFLYCNENGLLGSPS 420
DB 361 SMKQFLKAHRIVHKLFSLSKCKHQPLISLPRQRTSTTWLTRIQSFLYCNENGLLGSPS 420
QY 421 EETHSCTCPNDQVCTAFLEPCTVGDASACLTCPAPDNTRCGTCTGNTGMYLSSQGLCKEVAE 480
DB 421 EETHSCTCPNDQVCTAFLEPCTVGDASACLTCPAPDNTRCGTCTGNTGMYLSSQGLCKEVAE 480
QY 481 STDHYIGFETDLODLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRMLLTLSKN 540
DB 481 STDHYIGFETDLODLEMKYLLQKTDRIEIVHAFISNDMLNSWFDPSWKRMLLTLSKN 540
QY 541 KYKSSLVHMLILGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWPVSNSFPDWERTK 600
DB 541 KYKSSLVHMLILGLSLQCLTKNSTLEPLVAVYVNPFGGSHSFWPVSNSFPDWERTK 600
QY 601 LDLPLOQYNWTLTLGNKWKTFETVHIYLSRSIKNSGPNESIIYVEPLEFIDPSRNLYG 660
DB 601 LDLPLOQYNWTLTLGNKWKTFETVHIYLSRSIKNSGPNESIIYVEPLEFIDPSRNLYG 660
QY 661 MKINNIQVFGYSMHFDEPAIRDILQDYPYTOGSODSALLQLLEIRDRVNLSPPGQRR 720
DB 661 MKINNIQVFGYSMHFDEPAIRDILQDYPYTOGSODSALLQLLEIRDRVNLSPPGQRR 720
QY 721 LDLPFCLLRHRLKLSSTSEVVRISQALQAFNAKLPTNDYDITTKLCS 766
DB 721 LDLPFCLLRHRLKLSSTSEVVRISQALQAFNAKLPTNDYDITTKLCS 766

RESULT 3
Q8KIM7 PRELIMINARY; PRT; 766 AA.
ID Q8KIM7 AC Q8KIM7;
AC Q8KIM7;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE BMP/Retinoic acid-inducible neural-specific protein-3.
GN Name=BRINP3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RA Matsuoka I., Toda F., Nakatani T., Mori T., Ueno S., Kawano H.,
RA Kobayashi M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077854; BAC03100.1; -
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01823; MACPF, 1.
DR SMART; SM00181; EGF, 1.
DR SMART; SM00457; MACPF, 1.
SQ SEQUENCE 766 AA; 88496 MW; 0D2170F602E1BE5D CRC64;

Query Match          98.0%; Score 3998; DB 2; Length 766;
Best Local Similarity 97.7%; Pred. No. 2.1e-279;
Matches 748; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 MIWRRAGAEFLSMALMEWIALSLHCWLVAAVSDQHATSPFDWLLSDKGPFFHRSQY 60
DB 1 MIWRRAGAEFLSMALMEWIVLSLHCWLVAAVSDQHATSPFDWLLSDKGPFFHRSQY 60

QY 61 TDFVDRSQGSTRYKIYREFGRWKVNNLAVERRNPLGSPFLAPEFFRNIRLLGRRPTL 120
DB 61 TDFVDRSQGSTRYKIYREFGRWKVNNLAVERRNPLGSPFLAPEFFRNIRLLGRRPTL 120

QY 121 QOITENLIKKGTHFLSATLGGEESLTFVDKRLSKRAEGSDSTNSSSVTLTLHQL 180
DB 121 QOITENLIKKGTHFLSATLGGEESLTFVDKRLSKRPEGSETSTNSSSVTLTLHQL 180

QY 181 AASYFIDRDLRLRHIIQIATAIKVTETRTGPGCSNYDNLDSVSVLQSPENKIQ 240
DB 181 AASYFIDRDLRLRHIIQIATAIKVTETRTGPGCSNYDNLDSVSVLQSPENKIQ 240

QY 241 QGLQVLLPDYLOERFVQAALSVIACNSGEFTICKENDCWCCKGPKFPCNCPSMDIQ 300
DB 241 QGLQVLLPDYLOERFVQAALSVIACNSGEFTICKENDCWCCKGPKFPCNCPSMDIQ 300

QY 301 ENLIRITETWKAYNSDFESDEFLFMKRLPMNYELNTSTIMHLMTDSNFQRYEQL 360
DB 301 ENLIRITETWKAYNSDFESDEFLFMKRLPMNYELNTSTIMHLMTDSNFQRYEQL 360

QY 361 SMKQLFLKAHRIVHKLSLKRCHKQPLISLPRQRTSTYWLTRIOSFLYCNENGLLSFS 420
DB 361 SMKQLFLKAHRIVHKLSLKRCHKQPLISLPRQRTSTYWLTRIOSFLYCNENGLLSFS 420

QY 421 EETHSCTCPNDQVCTAFPLCTVGDASACLTCPADNRTRCGTCNTGYMLSQGLCKPEVAE 480
DB 421 EETHSCTCPNDQVCTAFPLCTVGDASACLTCPADNRTRCGTCNTGYMLSQGLCKPEVAE 480

QY 481 STDHYIGPETDLOLEMKYLLQKTDRIEVHAIPIFISNDMLNSWFPDPSWRKRMLLTLKSN 540
DB 481 STDHYIGPETDLOLEMKYLLQKTDRIEVHAIPIFISNDMLNSWFPDPSWRKRMLLTLKSN 540

QY 541 KYKSLVHMLGLSLQICLTKNSTLEPVLAVVNPFGGSHSESMPVNSFPDWERTK 600
DB 541 KYKSLVHMLGLSLQICLTKNSTLEPVLAVIINPFGGSHSESMPVNSFPDWERTK 600

QY 601 LDLPQCYNWTLTLGNKWKTFETVHIYLRISIKSNGPNSIESIYEPLEFIDPSRNLYG 660
DB 601 LDLPQCYNWTLTLGNKWKTFETVHIYLRISIKANGPNSIESIYEPLEFIDPSRNLYG 660

QY 661 MKINNIQVFGSMHFPDPAIRDILQLDYPYTOGSQDSALLQLLEIRDRVNKLSPQQR 720
DB 661 MKINNIQVFGSMHFPDPAIRDILQLDYPYTOGSQDSALLQLLEIRDRVNKLSPQQR 720

QY 721 LDLSCLLRHLRLKLSSTSVVRIQSAQAFNAKLPNTMDYDTTKLCS 766
DB 721 LDLSCLLRHLRLKLSSTSVVRIQSAQAFNAKLPNTVDYDTTKLCS 766

RESULT 4
Q6DFY8
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Db 312 DIQAMEDSLLOQDSWATHNRQFESEEFQTLKRLPDRFLNSTAISQVWTMDSNLQHR 371
QY 355 YEOLSNMQLFLKAKQIVHKLFSKRCCHKQPLISLPRQRTSTYWLTRIQSLYCNENG 414
Db 372 YQGLGASLVKLLKQWHRIVRRFLNCKRCHRPFRPLPKERSLSFWNRIQSLYCGEST 431
QY 415 LIGSFEETHSCTCPNDQVVTAFPLCTVGDASACLTCPADNRTRCGTCTNTGYMLSQGLC 474
Db 432 FPGTFLEQSHSCTCPYDQSSCOGPIPCALGEGPACAHACASDNSTRCGSNPGVYLAQGLC 491
QY 475 KPEVAESTHYIGFTDLOLEMKYLLQKTDRIEIVHAFISNDMLNSWFPDPSWKRML 534
Db 492 RPEVAESLENFLGLETDLQLELKYLLQKDRSRIEIVHSIFISNDMLGWSWFPDPSWKRML 551
QY 535 LTLKSNKYKSSLVHMLTGLQICLTKNSTLEPVLAVYVNPFGGSHSESWFMPVNSFP 594
Db 552 LTLKSNKYKPLVHVNLAUSLQICLTKNSTLEPVMAYVNPFGGSHSESWFMPVNEGNFP 611
QY 595 DWERTKLDLPLOQYNNWTLTGLNKKWKTFFETVHYILRSRIKSNPGNENESIYYEPLFIDP 654
Db 612 DWERTNVDAACQONWTLTGLNKKWKTFFETVHYILRSRIKSLDSSNETIYYEPLMTDP 671
QY 655 SNRLGYMKINNIQVFGSMHFDPEAIRDLILQDYPYTGQSODSALLQLELRDRVNKL 714
Db 672 SKNLGYMKINTLQVFGSYLFPDPAIRDLILQDYPYTGQSODSALLQLELRDRVNQLS 731
QY 715 PPGQRLDLFSCLLRHRLKLSSTSEVVRIOSSALQAFNAKLNTMDYDTTKLCS 766
Db 732 PPGKVRDLDFSCLLRHRLKLANNEVGRIQSSURAFNSKLNPVEYETGKLS 783

RESULT 5
O80T96 PRELIMINARY; PRT; 788 AA.
ID Q80T96
AC Q80T96;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKIAA1747 protein (Fragment).
GN Name=6430517E2IRik; Synonyms=MKIAA1747;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA genes:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
DR EMBL; AK122549; BAC65831.1; -
DR MGD; MGI:2443333; 6430517E2IRik.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
FT NON_TER
SQ SEQUENCE 788 AA; 89748 MW; DF4189DAFD43705B CRC64;

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Query Match 72.6%; Score 2963; DB 2; Length 788;
Best Local Similarity 70.7%; Pred. No. 9.2e-205;
Matches 546; Conservative 97; Mismatches 107; Indels 22; Gaps 5;
QY 17 LW-----EW-----TALSHCWVLAVAA-----VSDQHATS-----PFDWLLSDKGFPHRSQRY 60
DB 17 LWPEAPAPVALLALGVPGLVAVSATVAAVWPEQVSSAGAPLDWLLTDRGPFPHRAQRY 76

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QY 61 TDFVDRSGFSTRYKIYREFGRWKNVNLAVERRNPLSPFLAPEFFRNIRLLGRRPRL 120
Db 77 ADMEYRQGFTRIRYIYREFARWKNVNLALERRDFSLPLPLAPEFVNRIRLLGRPNL 136
QY 121 QOITENLIKKGTHFLSATLGGEESLTFVDRKRLSKRAEGSDSTT-----NSSSVTL 174
Db 137 QOVTEENLIKKGTHFLSATLGGEESLTFVDRKRLSKRAEGSETTGPIPVVGGPGNSAVSL 196
QY 175 ETLHOLAASYFDRDSTRRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSSVLVQSP 234
Db 197 ETLHOLAASYFDRDSTRRLRHIIQIASTAIKVTETRTGPGCSNYDNLDSVSSVLVQSP 256
QY 235 ENKIOLQGLVLLPYLQERFVQAAALSYIACNSEGEFFICKENDCWCCHGPKFPECNCPM 294
Db 257 ENKVQLLGLVLLPEHLRERFVAAALSYITCSSEGLVCRENDCKCKCSPTPECNCPDA 316
QY 295 DIOAMEENLLRITETWKAYNSDPESDFKLPMKRLPMNYFLNTSTIMHLWTMDSNFQRR 354
Db 317 DIOAMEDSLLOQDSWATHNRQFESEEFQTLKRLPDRFLNSTAISQVWTMDSNLQHR 376
QY 355 YBOLSNMQLFLKAKQIVHKLFSKRCCHKQPLISLPRQRTSTYWLTRIQSLYCNENG 414
Db 377 YQGLGASLVKLLKQWHRIVRRFLNCKRCHRPFRPLPKERSLSFWNRIQSLYCGEST 436
QY 415 LIGSFEETHSCTCPNDQVVTAFPLCTVGDASACLTCPADNRTRCGTCTNTGYMLSQGLC 474
Db 437 FPGTFLEQSHSCTCPYDQSSCOGPIPCALGEGPACAHACASDNSTRCGSNPGVYLAQGLC 496
QY 475 KPEVAESTHYIGFTDLOLEMKYLLQKTDRIEIVHAFISNDMLNSWFPDPSWKRML 534
Db 497 RPEVAESLENFLGLETDLQLELKYLLQKDRSRIEIVHSIFISNDMLGWSWFPDPSWKRML 556
QY 535 LTLKSNKYKSSLVHMLTGLQICLTKNSTLEPVLAVYVNPFGGSHSESWFMPVNSFP 594
Db 557 LTLKSNKYKPLVHVNLAUSLQICLTKNSTLEPVMAYVNPFGGSHSESWFMPVNEGNFP 616
QY 595 DWERTKLDLPLOQYNNWTLTGLNKKWKTFFETVHYILRSRIKSNPGNENESIYYEPLFIDP 654
Db 617 DWERTNVDAACQONWTLTGLNKKWKTFFETVHYILRSRIKSLDSSNETIYYEPLMTDP 676
QY 655 SNRLGYMKINNIQVFGSMHFDPEAIRDLILQDYPYTGQSODSALLQLELRDRVNKL 714
Db 677 SKNLGYMKINTLQVFGSYLFPDPAIRDLILQDYPYTGQSODSALLQLELRDRVNQLS 736
QY 715 PPGQRLDLFSCLLRHRLKLSSTSEVVRIOSSALQAFNAKLNTMDYDTTKLCS 766
Db 737 PPGKVRDLDFSCLLRHRLKLANNEVGRIQSSURAFNSKLNPVEYETGKLS 788

RESULT 6
O95560 PRELIMINARY; PRT; 781 AA.
ID O95560
AC O95560;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Rhodes S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035289; CAA22893.1; -
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
KW Hypothetical protein..
FT NON_TER

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RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RC	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Aletschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Mustalina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uesdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vallalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Matra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) .
RL	[2]
RC	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RA	Strausberg R.;
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RP	Inazawa J., Imoto I.;
RT	"Homo sapiens DBCCR1L2 mRNA for DBCCR1-like2.";
RT	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR	ENBL; BC028036; AH28036.1; -.
DR	ENBL; AB161694; BAD34946.1; -.
DR	InterPro; IPRO06210; IEFG.
DR	InterPro; IPRO01862; MAC_perforin.
DR	Pfam; PF01823; MACPF; 1.
DR	SMART; SM00181; EGF; 1.
DR	SMART; SM00457; MACPF; 1.
SQ	SEQUENCE 783 AA; 89004 MW; B8362095ADC97FCD CRC64;
	Query Match 72.6%; Score 2962; DB 2; Length 783;
	Best Local Similarity 70.6%; Pred. No. 1.1e-204;
	Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;
QY	16 ALWEW---IALSLHCWLVAIA-----VSDQHAT----SPFWLLSDKGPFHRSQBYTFP 63
Db	: :
Db	15 AVAPMTALLALGLPGWLVASATAAIVPEQHASVAGOHPLDWLLTDRGFFPHRAQEYADF 74
QY	64 VDRSGFTSTRYKIVREGRWKVNLAVERNFLGSLPLAPEFPFNRIELGRRPTLOOI 123
Db	: :
Db	75 MEYRQGFTTRVIIRYEFARWKVNLAERKDFLSLPPLAPEFINRIELGRRPNLQQV 134
QY	124 TENLIKKYGTHTFLSATLGGEESLTIFVDKRKLSKRAEGSDTT-----NSSSVTL 177
Db	: :
Db	135 TENLIKKYGTHTFLSATLGGEESLTIFVDKOKLGRKTETTGASIGGSNSTAVSLETL 194
QY	178 HQLAASYFDIRDSTLRRLHHIQIASTAIKVTRTGPGLCSNYDNLDSVSSLVQSPENK 237
Db	: :
Db	195 HQLAASYFDIRESTLRRLHHIQIATGAIKVTRETGPGLCSNYDNLDSVSSLVQSPENK 254
QY	238 IQIOGLQVLPPYLQERFVOAALSIIACNSEGEFTCKENDCHCGKPEPCNCPSMDITQ 297
Db	: :
Db	255 VQLGLQVLPPYLRFERFAAALSIIYCSESELVKENDCWCKCSPTPEPCNCPADITQ 314
QY	298 AMEENLRITETWKAYNSDFSDESFKLFMKRLPMNYFLTNTSTIHMLWTMDSGNFORRYEQ 357
Db	: :
Db	315 AMEDSLLQLQSWATHNQFESESEFOALLKKLPDDRFLNSTAI SQFWAMDTSLQHYVQ 374
QY	358 LENSMKQLPLKAQKIWHKLFSLSKCKHQPLISLPRTSTTWLTRI QSFLYCNEGLLG 417

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Db 375 LGAGLVKFKKTHRLRFLNLCRCHRPFRFLPKERSLSYWNRIQSLLYCGESTFPG 434
QY 418 SFSEETHSCPCNDQVCTAFLEPCTVGDASACLTCPADNTRCGTCTGWTGMLSQGLCKPE 477
Db 435 TFEQSHSCPCPYDQSCQCPICPACGEGPACAHCAPDNRTRCGSCNPGVYLAQGLCRPE 494
QY 478 VAEASTHYIGFETDLOLEMKYLLQKTDRIEIVHAFISNDMLNSGWFDPDSWRKMLLTL 537
Db 495 VAESLENFLGLETDLOLEKYLLOKDSRIEIVHSIFISNDMLNSGWFDPDSWRKMLLTL 554
QY 538 KSNKYKSSLVHMLIGLSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWFMVFNNSFPDWE 597
Db 555 KSNKYKPGLVHVMALSLQICLTKNSTLEPVMAYVNPFGGSHSSEWFMVFNNSFPDWE 614
QY 598 RTKLDLPLOCYNWTLTLGNKWKTFEETVHLYRSRISKSNCPNGNESIYIEPLEFIDPSRN 657
Db 615 RTNVDAACQONWTITLGNKWKTFEETVHLYRSRISKSLDSSNETIYIEPLEMTDPSKN 674
QY 658 LGYMKINNIQVFGYSMHFDPDAIRDILQLDYPTQGSQDSALLQLEIRDRVKNLSPPG 717
Db 675 LGYMKINTLVQVFGYSPFPDPAIRDILQLDYPTQGSQDSALLQLEIRDRVKNLSPPG 734
QY 718 QRLDLFSCLLRHRLKLSSTEVVRISQALQAFNAKLPNTMDYDTTKLCS 766
Db 735 KVRLLDLFSCLLRHRLKLANNEVGRIQSSIRAFNSKLPNPVEYETGKLCS 783

RESULT 8
Q8KIM8 PRELIMINARY; PRT; 783 AA.
AC Q8KIM8;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE BMP/Retinoic acid-inducible neurai-specific protein-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsushita I., Ueno S., Nakatani T., Toda F., Mori T., Kawano H.,
RA Kobayashi M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077853; BAC03099.1; -
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 783 AA; 89138 MW; 2FF2F9532F62975D CRC64;

Query Match 72.6%; Score 2962; DB 2; Length 783;
Best Local Similarity 70.7%; Pred. No. 1.1e-204;
Matches 546; Conservative 97; Mismatches 107; Indels 22; Gaps 5;

QY 17 LW-----EW-----IALSLHCWLVAA-----VSDQHATS-----PFDWLLSDKGFPHRSQY 60
Db 12 LWPEAAPWAVLLALGVPGWVAVSATVAAVVPEQHVSSAGAPLDWLLTDGPFPHRAQY 71
QY 61 TDFVDSRQGSFTRYKTYREFGKWNVLAVERNFLGSLPLAPEFNRILLGRPRTL 120
Db 72 ADMERYRQGFTRYRYIREFARWKNVLALEKDFSLPLPAPEFVNRILLGRPNL 131
QY 121 QQITENLIKYGTHFLLSATLGGEESLTI FVDRKRLSKRAEG-----SDSTNNSSVTL 174
Db 132 QQVTENLIKYGTHFLLSATLGGEESLTI FVDRKRLSKRSETLGGVVPVGGTGNSSAVSL 191
QY 175 ETIHLQAASYFIDRDSITRLRLHHIQASTAIAKVTETRTGPGLCGSDNVDLSDVSVLVQSP 234
Db 192 ETIHLQAASYFIDRSTRLRLHHIQATGAIKVTETRTGPGLCGSDNVDLSDVSVLVQSP 251

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QY 235 ENKIOLQGLVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCCHGCKPKPECCNCPSM 294
Db 252 ENKVQLGLQVLLPELHRERFVAALSYITCSEGLVCRENDWCCKSPFTFPECNCPDA 311
QY 295 DIQAMBEENLRITETWKAYNSDFEESDEFKJMKPLPMNYFLNTSTIMHLMTWDSNFQRR 354
Db 312 DIQAMEDSLQIODSWATHNRQFESEEFQTLKRLPSDRFLNSTAISQVWTMDANLQHR 371
QY 355 YQLENSMKQLFKAQKIVHKLFSLSKRCHKQPLSLPQRTSTYWLTIQSFYLYCNEG 414
Db 372 YOOLGASLVLLKXHVIRVRLFNLCRCHRPFRFLPKERSLSFWMNRIOQLLYCGEST 431
QY 415 LLGFSSEETHSCPCNDQVCTAFLEPCTVGDASACLTCPADNTRCGTCTGWTGMLSQGLC 474
Db 432 FPGTFLEQSHSCPCPYDQSCQCPICPACGEGPACAHCAASDNTTRCGSCNPGVYLAQGLC 491
QY 475 KPEVAESTDHYIGFETDLOLEMKYLLQKTDRIEIVHAFISNDMLNSGWFDPDSWRKML 534
Db 492 RPEVAESLENFLGLETDLOLEKYLLOKDSRIEIVHSIFISNDMLNSGWFDPDSWRKML 551
QY 535 LTLKSNKYKSSLVHMLIGLSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWFMVFNNSFP 594
Db 552 LTLKSNKYKPGLVHVMALSLQICLTKNSTLEPVMAYVNPFGGSHSSEWFMVFNNSFP 611
QY 595 DWERTKLDLPLOCYNWTLTLGNKWKTFEETVHLYRSRISKSNCPNGNESIYIEPLEFIDP 654
Db 612 DWERTNVDAACQONWTITLGNKWKTFEETVHLYRSRISKSLDSSNETIYIEPLEMTDP 671
QY 655 SRNLGYMKINNIQVFGYSMHFDPDAIRDILQLDYPTQGSQDSALLQLEIRDRVKNLS 714
Db 672 SRNLGYMKINTLVQVFGYSPFPDPAIRDILQLDYPTQGSQDSALLQLEIRDRVKNLS 731
QY 715 PPGQRLDLFSCLLRHRLKLSSTEVVRISQALQAFNAKLPNTMDYDTTKLCS 766
Db 732 PPGKVRLLDLFSCLLRHRLKLANNEVGRIQSSIRAFNSKLPNPVEYETGKLCS 783

RESULT 9
Q9C0B6 PRELIMINARY; PRT; 791 AA.
AC Q9C0B6;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE KIAA1747 protein (Fragment).
GN Name=KIAA1747;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:347-355(2000).
DR EMBL; AB051534; BAB21838.1; -
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
FT NON_TER
SQ SEQUENCE 791 AA; 89887 MW; 21C5CD35AAFC6A89 CRC64;

Query Match 72.6%; Score 2962; DB 2; Length 791;
Best Local Similarity 70.6%; Pred. No. 1.1e-204;
Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;

QY 16 ALWEW---IALSLHCWLVAA-----VSDQHAT-----SPFDWLLSDKGFPHRSQYTFP 63

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Db 23 AVAPWTALLALGLPGWVLAVSATAAAVVPQHASVAGQHPDLWLLTRDGRPFHRAQEVADF 82
QY 64 VDRSROGFSTRYKIYREFGRKWNVLAVRRNPLGSLPLAEPFFNIRLLGRPTLOI 123
Db 83 MEYRQGFTRIRYIREFARWKVNVALRERKDFSLPLAEPFIRNIRLLGRPNLOV 142
QY 124 TENLIKKYGTHFLLSATLGEESLTFVDRKRLSKRAEGSDSTT-----NSSSVTLETL 177
Db 143 TENLIKKYGTHFLLSATLGEESLTFVDRKRLSKRAEGSDSTT-----NSSSVTLETL 202
QY 178 HOLAAASYFDRDSTLRRLHHIQIASTAIKVTETRTPLGCSNYDNLDSSVSVLVQSPENK 237
Db 203 HOLAAASYFDRDSTLRRLHHIQIASTAIKVTETRTPLGCSNYDNLDSSVSVLVQSPENK 262
QY 238 IOLOGLQVLLPDYLOERFVOAALSYIACNSEGEFICKENDCHCQKPEPCNCPSMDIO 297
Db 263 VOLLLGLQVLLPYLRERFVAALSYITCSSEGLVCKENDCKCKSPTTPECCNPADLIQ 322
QY 298 AMEENLRITETWKAYNSDFEESDEFKLFMKRLPMNYFLTSTIMHLWTMDSNFORRYEQ 357
Db 323 AMEDSLLOQDSWATHNRQFESEEFQALLKRLPDRFLNSTAISQFWAMDTSLQHRVQQ 382
QY 358 LENSXKQPLKQAKIVHKLFSLSKCHQKPLISLPRQRTSTVWLTRIQSFLYCNENGLLG 417
Db 383 LGAGLKVLPKTHRIILRLFLNLCKRCHQRPRLPKERSLSYWNRIOSLLYCGESTFPG 442
QY 418 SFSEETHSCPCNDQVCTAFPLPCTVGDASACLTCAPONRTRCGTCNTGYMLSQGLCKPE 477
Db 443 TPLEQSHSCCTCYDSSQCGPIPCALGEGPACAHCAPDNSTRCGSCNPGYVLAQGLCKRPE 502
QY 478 VAESTDHYGFETDQLEMKYLLQKTDRIEVAHFIISNDMLNSWFDPSWRKMLLT 537
Db 503 VAESLENFLGLETDLQLEKYLLOKQDSRIEVSIFISNDMLNSWFDPSWRKMLLT 562
QY 538 KSNKYKSSLVHMLGLSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWE 597
Db 563 KSNKYKPLGVHMLALSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWE 622
QY 598 RTKLDLPQCYNWTITLGNKWKTFETVHIYLSRIKSGNPNESIIYEPLEFIDPSRN 657
Db 623 RTNVDAAQCCQNTITLGNRKWTFETVHVYLSRIKSLDSSNETIYIEPLEMTDPSKN 682
QY 658 LGYKMINNIQVGYSMHFDPAIRDLILQLDYPTQGSODSALLQLLEIRDRVNLSPGG 717
Db 683 LGYKMINNIQVGYSLPDPDAIRDLILQLDYPTQGSODSALLQLLEIRDRVNLSPGG 742
QY 718 QRRDLFSCLLRHLKLTSTSEVRIQSAQAFNAKLPTNMDYDTTKLCS 766
Db 743 KVRDLFSCLLRHLKLTSTSEVRIQSAQAFNAKLPTNMDYDTTKLCS 791

RESULT 10
Q6ZWC1
ID Q6ZWC1 PRELIMINARY; PRT; 678 AA.
AC Q6ZWC1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ41342.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,

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RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AKI23336; BAC85583.1; -.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 678 AA; 76520 MW; F34E4C754AC2612C CRC64;

Query Match 60.6%; Score 2474.5; DB 2; Length 678;
Best Local Similarity 70.5%; Pred. No. 1.3e-169;
Matches 451; Conservative 86; Mismatches 96; Indels 7; Gaps 2;

QY 133 THFLLSATLGEESLTFVDRKRLSKRAEGSDSTT-----NSSSVTLETLHQLAASYFI 186
Db 40 TNLVLFIT-GEESLTFVDRKRLSKRAEGSDSTT-----NSSSVTLETLHQLAASYFI 98
QY 187 DRDSTLRRLHHIQIASTAIKVTETRTPLGCSNYDNLDSSVSVLVQSPENKIQLOGLQVL 246
Db 99 DRESTLRRLHHIQIASTAIKVTETRTPLGCSNYDNLDSSVSVLVQSPENKIQLOGLQVL 158
QY 247 LPDYLOERFVOAALSYIACNSEGEFICKENDCHCQKPEPCNCPSMDIOAMEENLR 306
Db 159 LPEYLRERFVAALSYITCSSEGLVCKENDCKCKSPTTPECCNPADLIQIAMEDSLLOI 218
QY 307 TETWKAYNSDFEESDEFKLFMKRLPMNYFLTSTIMHLWTMDSNFORRYEQLENSXKQPL 366
Db 219 QDSWATHNRQFESEEFQALLKRLPDRFLNSTAISQFWAMDTSLQHRVQQGLCKRPE 278
QY 367 LKAKIVHKLFSLSKCHQKPLISLPRQRTSTVWLTRIQSFLYCNENGLLSFSSETHSC 426
Db 279 KKTTHRLRLFLNLCKRCHQRPRLPKERSLSYWNRIOSLLYCGESTFPGTFLQSHSC 338
QY 427 TCPNDQVCTAFPLPCTVGDASACLTCAPONRTRCGTCNTGYMLSQGLCKPEVAESTDHYI 486
Db 339 TCPYDSSQCGPIPCALGEGPACAHCAPDNSTRCGSCNPGYVLAQGLCKRPEVAESLENFL 398
QY 487 GFETDQLEMKYLLQKTDRIEVAHFIISNDMLNSWFDPSWRKMLLTLSKNYKSL 546
Db 399 GLETDQLEKYLLOKQDSRIEVSIFISNDMLNSWFDPSWRKMLLTLSKNYKPL 458
QY 547 VHMILGLSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWEKTLDPQ 606
Db 459 VHMILGLSLOICLTKNSTLEPVLAVYVNPFGGSHSSEWMPVNEGSFPDWEKTLDPQ 518
QY 607 CYNWTLTGNKWKTFETVHIYLSRIKSGNPNESIIYEPLEFIDPSRLNGYKMINNI 666
Db 519 CQNTITLGNRKWTFETVHVYLSRIKSLDSSNETIYIEPLEMTDPSKNLGYNKINTL 578
QY 667 QVFCYSMHFDPAIRDLILQLDYPTQGSODSALLQLLEIRDRVNLSPGQRRLDLPSC 726
Db 579 QVFCYSMHFDPAIRDLILQLDYPTQGSODSALLQLLEIRDRVNLSPGQRRLDLPSC 638

727 LLRHLKLTSTSEVRIQSAQAFNAKLPTNMDYDTTKLCS 766
639 LLRHLKLTSTSEVRIQSAQAFNAKLPTNMDYDTTKLCS 678

RESULT 11
Q7ZZR3
ID Q7ZZR3 PRELIMINARY; PRT; 761 AA.
AC Q7ZZR3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BMP/retinoic acid-inducible neural-specific protein.
GN Name=BRINP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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Db 587 WEKIRLQ-NSQCYNTWTLNLRNWKTFETVHLYRSKTRLPULLRNET-GQGPDVLSDFS 644
Qy 656 RNLYGKNNINIOVFGYSMEHDPFAIRDLILQLDYPTQSGQ-----DSALLQLELRDRVN 711
Db 645 KQFYIKISDVQVFGYSLRFNADLLRSVQVQVNSQYTOGGQFYSVSSSVMLLLIDIRDRIN 704
Qy 712 KLSP---PQORRLDLFSLRLHRLKLSSTSEVVRIOQALQAFNAKLNTMDYDTTKLC 765
Db 705 RLAPPVAPGPKQLDLFSCMLKHLKLTNSEIRVNHADLYNTEILKQSDQMTAKLC 761

RESULT 13
Q6PIAO PRELIMINARY; PRT; 761 AA.
AC Q6PIAO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Deleted in bladder cancer 1.
GN Name=DBC1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1] SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2] SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065196; AAHG5196.1;
DR InterPro; IPR001862; MACP_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00457; MACPF; 1.
SQ SEQUENCE 761 AA; 88760 MW; 16FF47082FD52252 CRC64;

Query Match 53.0%; Score 2161; DB 2; Length 761;
Best Local Similarity 52.3%; Pred. No. 5, 9e-147;
Matches 406; Conservative 134; Mismatches 209; Indels 28; Gaps 10;

Qy 1 MIMSRAGAEFLSMALMEWIALS-LHCWLVAAVSDQHATSPFDWLLSDKGFPHRSQE 59
Db 1 MNWRF--VELLYFLFWIGRISVQPSH---QEPAGTDQHVSKFDFWLISDRGFPHRS 53
Qy 60 YTDVDRSQGFSTRYKTYRFGWKNNLVAERNFLGSLPLAPFFRNIRLLGRPT 119
Db 54 YLSFVERHQGFTRTYKTYRFAWKVNTAIERDLVRHPVPLMPFQFSIRLLGRPT 113
Qy 120 LQQTENLIKKGTHFLLSATLGCEESLTFVDRKRLSKRAEGSDSTTNSSSVLTLELHQ 179
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Db 114 TQOFTDTIKKKGTHLLSATLGGSEALTMVMDKGR-----DRKSGNATQSVLALHQ 166
Qy 180 LAASYFIDRDSTLRLLHHIQIASTAIKVTETRTGPGCSYNDNLDSDSVSVLVQSPENKIQ 239
Db 167 LASSYFVDRDGTMRRLHEIQISTGAIKVTETRTGPGCSYNDNLDSDSVSVLVQSTESKLH 226
Qy 240 LOGQLVLLPDYLOERFVQAALSYIACNSEGEFICKENDCWCHGCKPFCPCNCPSMDIQAM 299
Db 227 LOGLOIIFPOYLQERFVQSALSYIMCNGEGEYLQNSQCRCQCAEEFPQCNCPITDIQIM 286
Qy 300 EENLLRITITWKAYNSDFEESDEFKLFMKRLPMNYFLNTSTIMHLWTMDSNFORRYEQLE 359
Db 287 EYTLANMAKSWAEAYKDLSENDEFASFPMKRLPSNHLFTIGSHQHWGNDWDQNRKLLQ 346
Qy 360 NSMKOLFKAQKIVHKLFSLSKRCCHKQPLISLPRQRTSTYMLTRIQSFLYCNENGLLSGF 419
Db 347 SATEAQRQKIORTARKLFLSVRCRHNPNHQLPRETTIQOMLARVQSLLYCNENGLFWGTF 406
Qy 420 SEETHSCCTCPNDVVCTAFPLCTVGDASACLTCPADNTRCGTCNTGYMLSGCLCKPEVA 479
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Qy 480 ES--TDHYIGFETDL--QDLEWKYLLQKTDRIEVEHAFISNDMLNSWDFDPSWRKRMLL 535
Db 467 DSESEQFISFETDLDFQDLKLLKYLQKMSRLYVHTTFISNEIRLDTFFDPRWRKMSL 526
Qy 536 TLKNKYKSSLVHMLGLSLQICLTSTLPEVLAVYVYVPGGSHSESWFMPVNSFPD 595
Db 527 TLKSNKRNMDFIHVMVIGMSRMCQWRNSLSDPMFPVYVYVPGGSHSESWFMPFGEFYPR 586
Qy 596 WERTKLDLPQCYNWTLLGNKWKTFETVHLYRSRISKSGNPGNENSIYIEPPLFIDPS 655
Db 597 WEKIRLQ-NSQCYNTWTLNLRNWKTFETVHLYRSRTRLPULLRNET-GQGPDVLSDFS 644
Qy 656 RNLYGKNNINIOVFGYSMEHDPFAIRDLILQLDYPTQSGQ-----DSALLQLELRDRVN 711
Db 645 KQFYIKISDVQVFGYSLRFNADLLRSVQVQVNSQYTOGGQFYSVSSSVMLLLIDIRDRIN 704
Qy 712 KLSP---PQORRLDLFSLRLHRLKLSSTSEVVRIOQALQAFNAKLNTMDYDTTKLC 765
Db 705 RLAPPVAPGPKQLDLFSCMLKHLKLTNSEIRVNHADLYNTEILKQSDQMTAKLC 761

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Q920P3 PRELIMINARY; PRT; 760 AA.
AC Q920P3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE BMP/retinoic acid-inducible neural-specific protein (BRINP) (Mus
DE musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE enriched library, clone:B230117A03 product:deleted in bladder cancer
DE chromosome region candidate 1 (human), full insert sequence) (Deleted
DE in bladder cancer chromosome region candidate 1).
GN Name=Dccrl; Synonyms=BRINP;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1] SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Matsuko I., Nakatani T., Kawano H., Kobayashi M., Matsumoto K.,
RA Ariga H., Abe A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[2] SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
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RL Meth. Enzymol. 303:19-44(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=20459374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RN Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RP "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=20459374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RN Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RP "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RN Konno H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RN Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,  
RN Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RP "RIKEN integrated sequence analysis (RISA) system-384-Format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RN Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RN Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RN Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RN Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RN Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Brain;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RN Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RN Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RN Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Umedin T.B., Toshikiyuki S., Carninci P., Prange C.,  
RN Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RN Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RN Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RN Jones S.J., Marra M.A.;  
RP "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Brain;  
RX Director MGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB060589; BAB70601.1; -;  
DR EMBL; AK045420; BAC32355.1; -;  
DR EMBL; BC079630; AAH79630.1; -;  
DR MGD; MGI:1928478; Dbccl1.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0005515; P:protein binding; ISS.  
DR GO; GO:0007049; P:cell cycle; ISS.  
DR GO; GO:0008219; P:cell death; ISS.  
DR Pfam; PF01823; MACPF; 1.  
DR SMART; SM00457; MACPF; 1.  
SQ SEQUENCE 760 AA, 88641 MW, 746E954368F1E49A CRC64;  
  
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Best Local Similarity 51.9%; Pred. No. 1.5e-146;  
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DB 55 LSFVERHQGFTRTYKTYREFARWVNTAIBRRDLVRHPVLPMPFQFSIRLLGRPTT 114  
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DB 115 QOFDITIIKYGTHLLISATLGGEALTYMDKSL-----DRKSGNATQSVEALHOL 167  
QY 181 AASYFIDRDSLTLLRHIIQIASTAIVTETRTGPGCSNDYDNLDSVSVLVOSPENKIOL 240  
DB 168 ASSYFVDRDGTMRRLHEIQISTGALKVTETRTGPGCSNDYDNLDSVSVLLSTESKLHL 227  
QY 241 QGLQVLLPDYLOERFVQAALSYIACNSEGEFTICKENDCWCCHGPKFPECNCPMDIQAME 300  
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QY 301 ENLLRITETKAYNSDFEESDEFKLFMKRLPNYPLNTSTIMHLMTDSNFORRYEQL 360  
DB 288 ETLANMAKAWTEAYKDLNSENDEFSFMKRLPSNHFLLTIGSIHOHWGNDWDLOSRYKLLOS 347  
QY 361 SMKQLFLKAKIVHKLFSLSKCHKQPLISLPRTSTYVLTTRIQSFLYCNENGLLGFS 420  
DB 348 ATEAQRQKIQTARKLFGLSVRCRNPHPQLPRETIQWLARVQSLLYCNENGFWTFL 407  
QY 421 EETHSCTCTPNDQVCTAFPLCTVGDASACLTCAPDNRTCTGTCNTGYMLSQGLCKPEVAE 480  
DB 408 ESQSCVCHGSGTTLCPPIIIGGNNSCAMCSLANISLCGSCNKGKLYRCRCEPQNV 467  
QY 481 S---TDHYIGFETDL---QDLEMKYLLOKTDRIEVHAIETSDNMLNSWFDPSWRKMLLT 536  
DB 468 SERSEQTSFETDLFDQLLEKYLQKMDSLRYVHTTETISNETRLDTFFDPPRRKMSLT 527  
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QY 597 ERTKLDLPQCYNWTLTLGNKWKTFETVHYLRSRIKSNNGNENSIYEPLEFIDPR 656  
DB 588 EKIRLQ-NSQCVNWTLLGNRWKTFETVHYLRSRTL--PTLRNETGQGVLDSDPSK 644  
QY 657 NLGYKNNIIVQGVGMHFDPEARDLLILDYPTQSQ-----DSALLQLEIDRVNK 712  
DB 645 ROFYIKISDVQVFGYSLRFNADLLRSVQVQNSQYTGQGFYSSSSVMLLMIDIRINR 704



Db 705 LAPPVAPGKQDLDFSCMLKHLKLTNSEIIRVNHADLYNTEILKQSDQMTAKLC 760

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